

Figure 1a

HAMGEN2520-59 Coding region and amino acid sequence.

Seq ID NO:

10	20	30	40	50	60
1 ATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTCCCTGTCCAGGAAGAAGCGGTTGGAG					
2 M R A T P L A A P A G S L S R K K R L E					
70 80 90 100 110 120					
TTGGATGACAACCTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCAG					
L D D N L D T E R P V Q K R A R S G P Q					
130 140 150 160 170 180					
CCCAGACTGCCCTGCCTGTTGCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACT					
P R L P P C L L P L S P P T A P D R A T					
190 200 210 220 230 240					
GCTGTGCCACTGCCTCCGTCTGGGCCCTATGTCCTCCTGGAGGCCGAGGAGGGCGGG					
A V A T A S R L G P Y V L L E P E E G G					
250 260 270 280 290 300					
CGGGCCTACCGGGCCCTGCACTGCCCTACAGGCACTGAGTATACCTGCAAGGTGTACCC					
R A Y R A L H C P T G T E Y T C K V Y P					
310 320 330 340 350 360					
GTCCAGGAAGCCCTGGCCGTGCTGGAGCCCTACGCGCGCTGCCCGCACAAAGCATGTG					
V Q E A L A V L E P Y A R L P P H K H V					
370 380 390 400 410 420					
GCTCGGCCACTGAGGTCTGGCTGGTACCCAGCTCCTCTACGCCTTTCACTCGGACC					
A R P T E V L A G T Q L L Y A F F T R T					
430 440 450 460 470 480					
CATGGGACATGCACAGCCTGGTGCAGGCCACCGTATCCCTGAGCCTGAGGGCTGCC					
H G D M H S L V R S R H R I P E P E A A					
490 500 510 520 530 540					
GTGCTCTCCGCCAGATGCCACCGCCCTGGCGCACTGTCACCAGCACGGTCTGGCCTG					
V L F R Q M A T A L A H C H Q H G L V L					
550 560 570 580 590 600					
CGTGATCTCAAGCTGTGCTGCTTGTCTCGCTGACCGTGAGAGGAAGAAGCTGGTCTG					
R D L K L C R F V F A D R E R K K L V L					
610 620 630 640 650 660					
GAGAACCTGGAGGAACCTCGCGTGACTGGGCCAGATGATTCCCTGAGGGACAAGCAC					
E N L E D S C V L T G P D D S L W D K H					
670 680 690 700 710 720					
GCGTGCCCTACGTGGACCTGAGATACTCAGCTCACGGCCTCATACTCGGGCAAG					
A C P A Y V G P E I L S S R A S Y S G K					
730 740 750 760 770 780					
GCAGCCGATGTCCTGGAGCCTGGCGCTGGCGCTCTTACCATGCTGGCCGGCACTACCC					
A A D V W S L G V A L F T M L A G H Y P					
790 800 810 820 830 840					
TTCCAGGACTCGGAGCCTGTCCTGCTCTCGGCAAGATCCGCCGCGGGCCTACGCC					
F Q D S E P V L L F G K I R R G A Y A L					
850 860 870 880 890 900					
CCTGCAGGCCCTCGGCCCTGCCCGCTGCTGGTCGCTGCCCTCGTCGGAGCCA					
P A G L S A P A R C L V R C L L R R E P					

Figure 1b

hAMGEN2520-59 Coding region and amino acid sequence
(continued).

Seq ID NO:

	910	920	930	940	950	960														
1	GCTGAA	CGG	CTCACAG	CCACAGG	CATCCT	CCTGCAC	CCCTGG	CTGCGAC	AGGAC	CCGATG										
2	A	E	R	L	T	A	T	G	I	L	L	H	P	W	L	R	Q	D	P	M
	970																	1010		1020
	CCCTT	AGCCCC	AAACCC	GATCCC	ATCTCT	GGGAGG	GCTGCC	CAGGTGG	TCCCTG	ATGG	ACTG									
	P	L	A	P	T	R	S	H	L	W	E	A	A	Q	V	V	P	D	G	L
	1030																	1060		1070
	GGG	CTGG	ACGA	AGCC	CAGG	GAAG	GGAG	AGGG	GAGA	CAG	GAGA	AGT	GGTT	CTGT	ATGG	CTAG				
	G	L	D	E	A	R	E	E	G	D	R	E	V	V	L	Y	G			

Figure 2a

1	50	2520-59	(1)	51	100
Genbank	BAB15597	(1)	(1)	(1)	MRATPLAAPAGSLSRKRRLELDDNLDT
Patented Seq:	NO 1367	(1)	(1)	(1)	MRATPLAAPAGSLSRKRRLELDDNLDT
Patented SEQ ID NO:	1102	(1)	(1)	(1)	MRATPLAAPAGSLSRKRRLELDDNLDT
JJ503-KS		(1)			MRATPLAAPAGSLSRKRRLELDDNLDT
Consensus		(1)			MRATPLAAPAGSLSRKRRLELDDNLDT
					150
Genbank	BAB15597	(1)	(1)	(1)	PPAGALEALSPGGARAHAERRGEMRATPLAAPAGSLSRKRRLELDDNLDT
Patented Seq:	NO 1367	(51)	(51)	(51)	PPAGALEALSPGGARAHAERRGEMRATPLAAPAGSLSRKRRLELDDNLDT
Patented SEQ ID NO:	1102	(1)	(1)	(1)	PPAGALEALSPGGARAHAERRGEMRATPLAAPAGSLSRKRRLELDDNLDT
JJ503-KS		(20)			PPAGALEALSPGGARAHAERRGEMRATPLAAPAGSLSRKRRLELDDNLDT
Consensus		(51)			PPAGALEALSPGGARAHAERRGEMRATPLAAPAGSLSRKRRLELDDNLDT
					101
Genbank	BAB15597	(28)	(28)	(28)	ERPVQKRARSQGPQPRLPPCILLPLSPPTAPDRATAVATASRLGPYVILLEPE
Patented Seq:	NO 1367	(28)	(28)	(28)	ERPVQKRARSQGPQPRLPPCILLPLSPPTAPDRATAVATASRLGPYVILLEPE
Patented SEQ ID NO:	1102	(101)	(101)	(101)	ERPVQKRARSQGPQPRLPPCILLPLSPPTAPDRATAVXTXSRXXXXVILLEEAR
JJ503-KS		(1)	(1)	(1)	ERPVQKRARSQGPQPRLPPCILLPLSPPTAPDRATAVATASRLGPYVILLEPE
Consensus		(70)			ERPVQKRARSQGPQPRLPPCILLPLSPPTAPDRATAVATASRLGPYVILLEPE
		(101)			ERPVQKRARSQGPQPRLPPCILLPLSPPTAPDRATAVATASRLGPYVILLEPE

Figure 2b

2520-59	151	EGGRAYRALHCPTGTTEYTCVKVPPVQEALALAVLEPYARLPPHKHVARPTEVL	200
Genbank BAB15597	(78)	EGGRAYQALHCPTGTTEYTCVKVPPVQEAPAVLEPYARLPPHKHVARPTEVL	
Patented Seq: NO 1367	(78)	RXA-----	
Patented SEQ ID NO:1102	(151)	-----	
Patented SEQ ID NO:1102	(1)	-----	GP
JJ503-KS	(120)	EGGRAYQALHCPTGTTEYTCVKVPPVQEALALAVLEPYARLPPHKHVARPTEVL	
Consensus	(151)	EGGRAYQALHCPTGTTEYTCVKVPPVQEALALAVLEPYARLPPHKHVARPTEVL	
	201	-----	250
2520-59	(128)	AGTQQLYAFFTRTHGDMHSLVRSRHRIPPEPEAAVLFRQMATALAHCHQHG	
Genbank BAB15597	(128)	AGTQQLYAFFTRTHGDMHSLVRSRHRIPPEPEAAVLFRQMATALAHCHQHG	
Patented Seq: NO 1367	(154)	-----	
Patented SEQ ID NO:1102	(3)	GWYPAPLRLFHSDPWGHQAQPGAKRHRIPPEPEAAVLFRQMATALAHCHQHG	
JJ503-KS	(170)	AGTQQLYAFFTRTHGDMHSLVRSRHRIPPEPEAAVLFRQMATALAHCHQHG	
Consensus	(201)	AGTQQLYAFFTRTHGDMHSLVRSRHRIPPEPEAAVLFRQMATALAHCHQHG	
	251	-----	300
2520-59	(178)	LVLRLDLKLCCRFFADRRERKKLVLENLEDSCVLTGPDDSLWDKHACCPAYVG	
Genbank BAB15597	(178)	LVLRLDLKLCCRFFADRRERKKLVLENLEDSCVLTGPDDSLWDKHACCPAYVG	
Patented Seq: NO 1367	(154)	-----	
Patented SEQ ID NO:1102	(53)	LVLRLDLKLCCRFFADRRERKKLVLENLEDSCVLTGPDDSLWDKHACCPAYVG	
JJ503-KS	(220)	LVLRLDLKLCCRFFADRRERKKLVLENLEDSCVLTGPDDSLWDKHACCPAYVG	
Consensus	(251)	LVLRLDLKLCCRFFADRRERKKLVLENLEDSCVLTGPDDSLWDKHACCPAYVG	
	301	-----	350
2520-59	(228)	PEILSSRASYSGKAADVWSLGVALFTMLLAGHYPFQDSEPVLLFGKIRRGA	
Genbank BAB15597	(228)	PEILSSRASYSGKAADVWSLGVALFTMLLAGHYPFQDSEPVLLFGKIRRGA	
Patented Seq: NO 1367	(154)	-----	
Patented SEQ ID NO:1102	(103)	PEILSSRASYSGKAADVWSLGVALFTMLLAGHYPFQDSEPVLLFGKIRRGA	
JJ503-KS	(270)	PEILSSRASYSGKAADVWSLGVALFTMLLAGHYPFQDSEPVLLFGKIRRGA	
Consensus	(301)	PEILSSRASYSGKAADVWSLGVALFTMLLAGHYPFQDSEPVLLFGKIRRGA	

Figure 2c

2520-59	351	(278) YALPAGLSAPARCLVRCLLRRPAERLTATGILLHPWLQRDPMPPLAPTRS	400
Genbank BAB15597	(278)	YALPAGLSAPARCLVRCLLRRPAERLTATGILLHPWLQRDPMPPLAPTRS	
Patented Seq: NO 1367	(154)	-	
Patented SEQ ID NO:1102	(153)	YALPAGLSAPARCLVRCLLRRPAERLTATGILLHPWLQRDPMPPLAPTRS	
JJ503 -KS	(320)	YALPAGLSAPARCLVRCLLRRPAERLTATGILLHPWLQRDPMPPLAPTRS	
Consensus	(351)	YALPAGLSAPARCLVRCLLRRPAERLTATGILLHPWLQRDPMPPLAPTRS	
2520-59	401		431
Genbank BAB15597	(328)	HLWEAAQVVPDGLGLDEAREEEGDRREVVLYG	
Patented Seq: NO 1367	(154)	-	
Patented SEQ ID NO:1102	(203)	HLWEAAQVVPDGLGLDEAREEEGDRREVVLYG	
JJ503 -KS	(361)	-	
Consensus	(401)	HLWEAAQVVPDGLGLDEAREEEGDRREVVLYG	